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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/045,815

DATE: 05/02/2002 P.6
TIME: 15:43:53

Input Set : A:\06501-091001.TXT
Output Set: N:\CRF3\05022002\J045815.raw

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 4 <110> APPLICANT: Wadhwa, Renu
 5         Sugihara, Takashi
 6         Ohide, Akiko
 8 <120> TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
10 <130> FILE REFERENCE: 06501-091001
12 <140> CURRENT APPLICATION NUMBER: US 10/045,815
13 <141> CURRENT FILING DATE: 2001-10-26
15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/02731
16 <151> PRIOR FILING DATE: 2000-04-26
18 <150> PRIOR APPLICATION NUMBER: JP 11/118806
19 <151> PRIOR FILING DATE: 1999-04-26
21 <160> NUMBER OF SEQ ID NOS: 15
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2829
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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36                                                              Met Ala
37                                                              1
39 gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg gcc gct    105
40 Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val Ala Ala
41          5                  10                  15
43 gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg gtg acg    153
44 Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met Val Thr
45          20                  25                  30
47 cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac    201
48 Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp
49   35                  40                  45                  50
51 tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca    249
52 Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala
53                  55                  60                  65
55 gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac    297
56 Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp
57                  70                  75                  80
59 ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc    345
60 Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala
61                  85                  90                  95
63 tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg    393
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64 Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu
65     100                 105             110
67 cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac    441
68 Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His
69 115             120             125             130
71 tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc ccc tac    489
72 Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr
73             135             140             145
75 aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct    537
76 Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala
77             150             155             160
79 gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa    585
80 Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu
81         165             170             175
83 atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag    633
84 Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu
85     180             185             190
87 gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga    681
88 Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg
89 195             200             205             210
91 ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc    729
92 Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro
93             215             220             225
95 cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc    777
96 His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys
97             230             235             240
99 cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt    825
100 Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu
101         245             250             255
103 gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag    873
104 Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln
105     260             265             270
107 gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca    921
108 Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro
109 275             280             285             290
111 agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat    969
112 Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr
113             295             300             305
115 ctg cag ttt gcc tac tat aac att ggg aat tat aca caa gct ggt gaa    1017
116 Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala Gly Glu
117             310             315             320
119 tgt gcc aag acc tat ctt ctc ttc ttc ccc aat gac gag gtg atg aac    1065
120 Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val Met Asn
121         325             330             335
123 caa aat ttg gcc tat tat gca gct atg ctt gga gaa gaa cac acc aga    1113
124 Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His Thr Arg
125     340             345             350
127 tcc atc ggc ccc cgt gag cag ggc acc tagggaaaga tgtgaccccg         1160
128 Ser Ile Gly Pro Arg Glu Gln Gly Thr
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129 355                    360
131 gaaagtactc agtttccctg ccctggagtg ccaaggagta ccgacagcga agcctactgg   1220
132 aaaaagaact gctttttcttc gcttatgatg ttttttggaat tccctttgtg gatcgggatt   1280
133 catggactcc agaagaaatg attcccaaga aattgcaaga gaaacagaag tgaggacctt   1340
134 gaagaaactg catggttgga tcagtctgat gaagcacttg aggcttcttg agcccaggca   1400
135 gatgtgaact cctggcaagg ggtgggcagg tccagtttgg gaagtcgggg tggagcccag   1460
136 ggctggccct ggaatgcagt cctcagagcg gttgtgctca taggtcagaa cgggaaacag   1520
137 ccgtacgcat ctcccaggag attgggaacc ttatgaagga aatcgagacc cttgtggaag   1580
138 agaagaccaa ggagtcactg gatgtgagca gactgacccg ggaaggtggc ccctgctgt   1640
139 atgaaggcat cagtctcacc atgaactcca aactcctgaa tggttaccag cgggtggtga   1700
140 tggacggcgt aatctctgac cacgagtgtc aggagctgca gagactgacc aatgtggcag   1760
141 caacctcagg agatggctac cggggtcaga cctccccaca tactcccaat gaaaagttct   1820
142 atggtgtcac tgtcttcaaa gccctcaagc tggggcaaga aggcaaagtt cctctgcaga   1880
143 gtgcccacct gtactacaac gtgacggaga aagtgcggcg catcatggag tcctacttcc   1940
144 gcctggatac gcccctctac ttttcctact ctcatctggt gtgccgcact gccatcgaag   2000
145 aggtccaggc agagaggaag gatgatagtc atccagtcca cgtggacaac tgcatcctga   2060
146 atgccgagac cctcgtgtgt gtcaaagagc ccccagccta caccttccgc gactacagcg   2120
147 ccatcctta cctaaatggg gacttcgatg gcggaaactt ttatttcact gaactggatg   2180
148 ccaagaccgt gacggcagag gtgcagcctc agtgtggaag agccgtggga ttctcttcag   2240
149 gcactgaaaa cccacatgga gtgaaggctg tcaccagggg gcagcgctgt gccatcgccc   2300
150 tgtggttcac cctggaccct cgacacagcg agcgggacag ggtgcaggca gatgacctgg   2360
151 tgaagatgct cttcagccca gaagagatgg acctctccca ggagcagccc ctggatgccc   2420
152 agcagggccc ccccgaacct gcacaagagt ctctctcagg cagtgaatcg aagcccaagg   2480
153 atgagctatg acagcgtcca ggtcagacgg atgggtgact agacccatga agaggaactc   2540
154 ttcttgcact ctgagctggc cagcccctcg gggctgcaga gcagtgagcc tacatctgcc   2600
155 actcagccga ggggaccctg ctcacagcct tctacatggt gctactgctc ttggagtgga   2660
156 catgaccaga caccgcaccc cctggatctg gctgagggct caggacacag gcccagccac   2720
157 ccccaggggc ctccacaggc cgctgcataa cagcgataca gtacttaagt gtctgtgtag   2780
158 acaaccaaag aataaatgat tcatggtttt ttttaaaaaa aaaaaaaa            2829
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 363
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166 Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
167 1               5                   10                  15
168 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
169               20                  25                  30
170 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
171           35                  40                  45
172 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
173       50                  55                  60
174 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
175 65                  70                  75                  80
176 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
177               85                  90                  95
178 Gln Ala Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
179               100                 105                 110
180 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
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181           115                   120                   125
182 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
183       130                   135                   140
184 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu
185 145                   150                   155                   160
186 Lys Ala Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His
187             165                   170                   175
188 Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val
189           180                   185                   190
190 Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu
191       195                   200                   205
192 Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala
193       210                   215                   220
194 Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu
195 225                   230                   235                   240
196 Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn
197             245                   250                   255
198 Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr
199           260                   265                   270
200 Ile Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser
201       275                   280                   285
202 His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr
203       290                   295                   300
204 Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala
205 305                   310                   315                   320
206 Gly Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val
207             325                   330                   335
208 Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His
209           340                   345                   350
210 Thr Arg Ser Ile Gly Pro Arg Glu Gln Gly Thr
211       355                   360
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214 <211> LENGTH: 2600
215 <212> TYPE: DNA
216 <213> ORGANISM: Homo sapiens
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (52)...(2259)
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225                                                             1
227 gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg gcc gct     105
228 Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val Ala Ala
229           5                   10                  15
231 gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg gtg acg     153
232 Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met Val Thr
233       20                  25                  30
235 cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac     201
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236 Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp
237  35                      40                  45                  50
239 tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca      249
240 Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala
241                      55                  60                  65
243 gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac      297
244 Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp
245                      70                  75                  80
247 ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc      345
248 Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala
249                      85                  90                  95
251 tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg      393
252 Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu
253      100                 105                 110
255 cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac      441
256 Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His
257 115                 120                 125                 130
259 tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc ccc tac      489
260 Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr
261                 135                 140                 145
263 aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct      537
264 Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala
265              150                 155                 160
267 gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa      585
268 Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu
269      165                 170                 175
271 atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag      633
272 Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu
273      180                 185                 190
275 gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga      681
276 Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg
277 195                 200                 205                 210
279 ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc      729
280 Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro
281                 215                 220                 225
283 cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc      777
284 His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys
285              230                 235                 240
287 cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt      825
288 Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu
289              245                 250                 255
291 gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag      873
292 Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln
293      260                 265                 270
295 gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca      921
296 Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro
297 275                 280                 285                 290
299 agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat      969
300 Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/02/2002
PATENT APPLICATION: US/10/045,815   TIME: 15:43:54

Input Set : A:\06501-091001.TXT
Output Set: N:\CRF3\05022002\J045815.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2376
Seq#:7; N Pos. 2282

VERIFICATION SUMMARY   DATE: 05/02/2002
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Input Set : **A:\06501-091001.TXT**
Output Set: **N:\CRF3\05022002\J045815.raw**

L:530 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2372
L:837 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2227